

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/713,928ADATE: 12/31/96
TIME: 10:32:19

INPUT SET: S14725.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANT: RADIN, DAVID N.
CRAMER, CAROLE L.
OISHI, KAREN K.
WEISSENBORN, DEBORAH L.

(ii) TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN
PLANT-BASED EXPRESSION SYSTEMS

(iii) NUMBER OF SEQUENCES: 12

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Pennie & Edmonds
(B) STREET: 1155 Avenue of the Americas
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: USA
(F) ZIP: 10036-2711

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/003,737
(B) FILING DATE: 14-SEP-1995

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Coruzzi, Laura A.
(B) REGISTRATION NUMBER: 30,742
(C) REFERENCE/DOCKET NUMBER: 7956-0011-999

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (212) 790-9090
(B) TELEFAX: (212) 869-9741
(C) TELEX: 66141 PENNIE

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47

48

49 (2) INFORMATION FOR SEQ ID NO:1:

50

51 (i) SEQUENCE CHARACTERISTICS:

52 (A) LENGTH: 27 base pairs

53 (B) TYPE: nucleic acid

54 (C) STRANDEDNESS: single

55 (D) TOPOLOGY: unknown

56

57 (ii) MOLECULE TYPE: other nucleic acid

58 (A) DESCRIPTION: /desc = "PCR primer"

59

60

61

62

63 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

64

65 TTGTCTAGAG TAAGCATCAT GGCTGGC

27

66

67 (2) INFORMATION FOR SEQ ID NO:2:

68

69 (i) SEQUENCE CHARACTERISTICS:

70 (A) LENGTH: 33 base pairs

71 (B) TYPE: nucleic acid

72 (C) STRANDEDNESS: single

73 (D) TOPOLOGY: unknown

74

75 (ii) MOLECULE TYPE: other nucleic acid

76 (A) DESCRIPTION: /desc = "PCR primer"

77

78

79

80

81 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

82

83 CACGAATTCT GGCGACGCCA CAGGTAGGTG TGA

33

84

85 (2) INFORMATION FOR SEQ ID NO:3:

86

87 (i) SEQUENCE CHARACTERISTICS:

88 (A) LENGTH: 1642 base pairs

89 (B) TYPE: nucleic acid

90 (C) STRANDEDNESS: unknown

91 (D) TOPOLOGY: unknown

92

93 (ii) MOLECULE TYPE: cDNA

94

95

96

97

98 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

99

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PATENT APPLICATION US/08/713,928ADATE: 12/31/96
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100	ATGGAGTTT CAAGTCCTT CAGAGAGGAA TGTCCCAAGC CTTTGAGTAG GGTAAGCATC	60
101		
102	ATGGCTGGCA GCCTCACAGG TTTGCTTCTA CTTCAGGCAG TGTCGTGGGC ATCAGGTGCC	120
103		
104	CGCCCCTGCA TCCCTAAAAG CTTGCGGTAC AGCTCGGTGG TGTGTGTCTG CAATGCCACA	180
105		
106	TACTGTGACT CCTTTGACCC CCCGACCTTT CCTGCCCTTG GTACCTTCAG CCGCTATGAG	240
107		
108	AGTACACGCA GTGGGCGACG GATGGGGCTG AGTATGGGGC CCATCCAGGC TAATCACACG	300
109		
110	GGCACAGGCC TGCTACTGAC CCTGCAGCCA GAACAGAAGT TCCAGAAAGT GAAGGGATTT	360
111		
112	GGAGGGGCCA TGACAGATGC TGCTGCTCTC AACATCCTTG CCCTGTCACC CCCTGCCCAA	420
113		
114	AATTTGCTAC TTAAATCGTA CTTCTCTGAA GAAGGAATCG GATATAACAT CATCCGGGTA	480
115		
116	CCCATGGCCA GCTGTGACTT CTCCATCCGC ACCTACACCT ATGCAGACAC CCCTGATGAT	540
117		
118	TTCCAGTTGC ACAACTTCAG CCTCCCAGAG GAAGATACCA AGCTCAAGAT ACCCCTGATT	600
119		
120	CACCGAGCCC TGCAGTTGGC CCAGCGTCCC GTTTCACTCC TTGCCAGCCC CTGGACATCA	660
121		
122	CCCACTTGGC TCAAGACCAA TGGAGCGGTG AATGGGAAGG GGTCAC TCAA GGGACAGCCC	720
123		
124	GGAGACATCT ACCACCAGAC CTGGGCCAGA TACTTTGTGA AGTTCCTGGA TGCCTATGCT	780
125		
126	GAGCACAAGT TACAGTTCTG GGCAGTGACA GCTGAAAATG AGCCTTCTGC TGGGCTGTTG	840
127		
128	AGTGGATACC CCTTCCAGTG CCTGGGCTTC ACCCCTGAAC ATCAGCGAGA CTTCATTGCC	900
129		
130	CGTGACCTAG GTCCTACCCT CGCCAACAGT ACTCACCACA ATGTCCGCCT ACTCATGCTG	960
131		
132	GATGACCAAC GCTTGCTGCT GCCCCACTGG GCAAAGGTGG TACTGACAGA CCCAGAAGCA	1020
133		
134	GCTAAATATG TTCATGGCAT TGCTGTACAT TGGTACCTGG ACTTTCTGGC TCCAGCCAAA	1080
135		
136	GCCACCCTAG GGGAGACACA CCGCCTGTTC CCAACACCA TGCTCTTTGC CTCAGAGGCC	1140
137		
138	TGTGTGGGCT CCAAGTTCTG GGAGCAGAGT GTGCGGCTAG GCTCCTGGGA TCGAGGGATG	1200
139		
140	CAGTACAGCC ACAGCATCAT CACGAACCTC CTGTACCATG TGGTCGGCTG GACCGACTGG	1260
141		
142	AACCTTGCCC TGAACCCCGA AGGAGGACCC AATTGGGTGC GTAAC TTTGT CGACAGTCCC	1320
143		
144	ATCATTGTAG ACGTCACCAG GGACACGTTT TACAAACAGC CCATGTTCTA CCACCTTGGC	1380
145		
146	CACTTCAGCA AGTTCATTCC TGAGGGCTCC CAGAGAGTGG GGCTGGTTGC CAGTCAGAAG	1440
147		
148	AACGACCTGG ACGCAGTGGC ACTGATGCAT CCCGATGGCT CTGCTGTTGT GGTCGTGCTA	1500
149		
150	AACCGCTCCT CTAAGGATGT GCCTCTTACC ATCAAGGATC CTGCTGTGGG CTTCTTGGAG	1560
151		
152	ACAATCTCAC CTGGCTACTC CATTCACACC TACCTGTGGC GTCGCCAGAA TTCGGACTAC	1620

RAW SEQUENCE LISTING PATENT APPLICATION US/08/713,928A

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153

154 AAGGACGACG ATGACAAAGTT GA

1642

155

156 (2) INFORMATION FOR SEQ ID NO:4:

157

158 (i) SEQUENCE CHARACTERISTICS:

159 (A) LENGTH: 546 amino acids

160 (B) TYPE: amino acid

161 (C) STRANDEDNESS: single

162 (D) TOPOLOGY: unknown

163

164 (ii) MOLECULE TYPE: peptide

165

166

167

168

169 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

170

171 Met Glu Phe Ser Ser Pro Ser Arg Glu Glu Cys Pro Lys Pro Leu Ser

172 1 5 10 15

173

174 Arg Val Ser Ile Met Ala Gly Ser Leu Thr Gly Leu Leu Leu Leu Gln

175 20 25 30

176

177 Ala Val Ser Trp Ala Ser Gly Ala Arg Pro Cys Ile Pro Lys Ser Phe

178 35 40 45

179

180 Gly Tyr Ser Ser Val Val Cys Val Cys Asn Ala Thr Tyr Cys Asp Ser

181 50 55 60

182

183 Phe Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr Phe Ser Arg Tyr Glu

184 65 70 75 80

185

186 Ser Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly Pro Ile Gln

187 85 90 95

188

189 Ala Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln

190 100 105 110

191

192 Lys Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala

193 115 120 125

194

195 Ala Leu Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu

196 130 135 140

197

198 Lys Ser Tyr Phe Ser Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val

199 145 150 155 160

200

201 Pro Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp

202 165 170 175

203

204 Thr Pro Asp Asp Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp

205 180 185 190

RAW SEQUENCE LISTING PATENT APPLICATION *US/08/713,928A*

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206	
207	Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln
208	195 200 205
209	
210	Arg Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu
211	210 215 220
212	
213	Lys Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro
214	225 230 235 240
215	
216	Gly Asp Ile Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu
217	245 250 255
218	
219	Asp Ala Tyr Ala Glu His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu
220	260 265 270
221	
222	Asn Glu Pro Ser Ala Gly Leu Leu Ser Gly Tyr Pro Phe Gln Cys Leu
223	275 280 285
224	
225	Gly Phe Thr Pro Glu His Gln Arg Asp Phe Ile Ala Arg Asp Leu Gly
226	290 295 300
227	
228	Pro Thr Leu Ala Asn Ser Thr His His Asn Val Arg Leu Leu Met Leu
229	305 310 315 320
230	
231	Asp Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val Leu Thr
232	325 330 335
233	
234	Asp Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr
235	340 345 350
236	
237	Leu Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg
238	355 360 365
239	
240	Leu Phe Pro Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser
241	370 375 380
242	
243	Lys Phe Trp Glu Gln Ser Val Arg Leu Gly Ser Trp Asp Arg Gly Met
244	385 390 395 400
245	
246	Gln Tyr Ser His Ser Ile Ile Thr Asn Leu Leu Tyr His Val Val Gly
247	405 410 415
248	
249	Trp Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu Gly Gly Pro Asn Trp
250	420 425 430
251	
252	Val Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Val Thr Lys Asp
253	435 440 445
254	
255	Thr Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys
256	450 455 460
257	
258	Phe Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/713,928A

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Original Text